

```

RESULT      8
W37712
ID    W37712 standard; Protein; 1106 AA.
XX
AC    W37712;
XX
DT    11-MAR-1998 (first entry)
XX
DE    Rabbit skeletal calcium channel alpha-2 subunit.
XX
KW    Rabbit; skeletal; calcium channel alpha-2 subunit; hybridisation;
KW    probe.
XX
OS    Oryctolagus cuniculus.
XX
PN    US5686241-A.
XX
PD    11-NOV-1997.
XX
PF    28-SEP-1994; 94US-0314083.
XX
PR    08-NOV-1990; 90US-0603751.
PR    04-APR-1988; 88US-0176899.
PR    04-APR-1989; 89WO-US01408.
PR    13-JUL-1992; 92US-0914231.
PR    28-SEP-1994; 94US-0314083.
XX
PA    (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI    Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME;
XX
DR    WPI; 1997-558134/51.
DR    N-PSDB; T96812.
XX
PT    Oligonucleotide probes - for identifying calcium channel alpha-2
PT    subunits
XX
PS    Disclosure; Fig 2A-F; 44pp; English.
XX
CC    This is a rabbit skeletal muscle calcium channel alpha-2 subunit.
CC    The DNA sequences of the alpha-2 subunit (rabbit and human -
CC    see T96812-13) are useful as hybridisation probes for identifying nucleic
CC    acids encoding all or part of a calcium channel alpha-2 subunit. Certain
CC    diseases, e.g. Lambert-Eaton Syndrome, involve autoimmune interactions
CC    with calcium channels. The ready availability of calcium channel subunits
CC    would make possible immunoassays for diagnosis of such diseases and an
CC    understanding of them at the molecular level that could lead to effective
CC    methods for treating them.
XX
SQ    Sequence 1106 AA;

```

Query Match 20.3%; Score 1148.5; DB 18; Length 1106;
Best Local Similarity 28.5%; Pred. No. 1.7e-88;
Matches 320; Conservative 234; Mismatches 440; Indels 129; Gaps 39;

Qy	33	SEQQIPLSV-VKLWASAFGGEIKSIAAKYSGSQQLLKKYKEYEKDVAIEEIDGLQLVKKL	91
Db	25	seepfpsavtikswvdkmqedlvltaktasgvnqlvdiyekyqdltytevpnnarqlveia	84
Qy	92	AKNMEEMFHKKSEAVRRLVEAAEEAHLKHEFDADL--QYEFYNAVLINERDKGNFLEL	148
Db	85	ardieklslsnrskalvrlaleaekvqaahqwredfasnevvyynak--ddldpekndsep	142
Qy	149	GKEFI--LAPNDHFNNLPVNISLSDVQVPTNMYNKDPAINVGWYWSESLNKVFVDNFDRD	206
Db	143	gsgrikpvfiddanfrqrvsyqhaavhiptdiyegstivlnelnwtsalddvfkknreed	202
Qy	207	PSLIWQYFGSAKGFFRQYPGIKWEPDE---NGVIAFDCRNKRWYIQAATSPKDVVILVDV	263
Db	203	psllwqvfqsatqlaryypaspwvdsrtpnkidlydvrrrrpwyiqqaaspkdmllivdv	262

Qy 264 SGSMKGLRLTIKQTVSSILDTLGDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHF 323
 Db 263 sgsvsgltklirtsvsemltlddddsvfnvasfnnaqdvscfq-hlvqanvrnkklv 320

Qy 324 REHLDKLFAKGIGMLDIALNEAFNLSDFNHTGQSICSQAIMLITDGAVDTYDTIFAKY 383
 Db 321 kdavnnitakgitdykkgfsafeqllnynvsran--cnkiimlftdggeeraqeifaky 378

Qy 384 NWPDRKVRIFTYLIGREAAFDNLKWMACANKGFFTQISTLADVQENVMEYLHVLSPKV 443
 Db 379 n-kdkkvrvtfsvgqhnydrpgiqwmacenkgyyeipsigairintqeyldvlgrpmv 437

Qy 444 I--DQEHVVWTEAYIDSTLTDQGPVLMTTVAMPVFS---KQNETRSKG-ILLGVVGT 496
 Db 438 lagdkakqvqwtvnyldal---elg--lvitgtlpvfnitgqfenktnknqlilgvmgv 492

Qy 497 DVPVKELLKTIPKYKLGHYAFAITNNGYILTHPELRL-----LYEEGKKRRKPNYSS 550
 Db 493 dvsledikrltprftlcpngyyfaidpnyvllhpnlpkpkigvgiptinlrkrpvnqn 552

Qy 551 -----VDLSEVEWEDRDDV---LRNAMVNRKTGK--FSMEVK----KTVDKGRVLMVT 595
 Db 553 pksqepvtldfldaelendikveirnkmidgesgektfrtlvksqderyidkgnrt---- 608

Qy 596 NDYYTIDIKGTFPSLGVALSRRGHGKYFFRGNVTIEEGLHDLHPDVSLADEW----- 647
 Db 609 --ytwtpvngtdysslalvltptysfyikak--ieetitqarysetlkpdnfeesgytfl 664

Qy 648 ---SYCNTDLHPEHRHLSQLEAIKLYLKGKEP-LLQCDKELIQEVLFDA-VVSAPIEAYW 702
 Db 665 aprdyc-sdlkpsdntefllnfnefidrktpnpscntdlinrvlldagftnelvqnyw 723

Qy 703 TSLALNKSSENSDKGVEVAFGLTRTGLSRINLFVGAELTNQDFLKAGDKENIFNADHFPL 762
 Db 724 s-----kqknikgvkarfvvtdggitrryp-----keagenwqenpetyeds 765

Qy 763 WYRRAAEQIPGSFVYSIPF--STGPVNKSNVVTASTSIQLLDERKSPVVAAGIQMKLEF 820
 Db 766 fykrsldn--dnyvftapyfnksgpgayesgimvskaveiyiqgkllkpavvgikidvns 823

Qy 821 FORKFWTASRQCASLDGKCSISCDDETVNICYLIDNNGFILVS--EDYT-QTGDFGEGIEG 877
 Db 824 wienftktsirdpcagpvcdckrnsdvmdcvilddggfllmanhddytnqigrffgeidp 883

Qy 878 AVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPY-----NAFLSAVKW 927
 Db 884 slmrhlvnisvyafnksydyqsvcepgaapkqga-ghrsayvpsiadilqigwwataaaw 942

Qy 928 IMTELVLFLVEF---NLCSWWHSDMTAKAQLKQTLPCDTEYPAFVSERTIKETGNI 983
 Db 943 silqqfllsltfprlleaadmedddftasmk-----qsciteqtqyffndsksfsgvl 997

Qy 984 ACEDCSKSFVIQQIPSSNLFMVVDS--SCLCESVAPITMAPIEIRYNESLKERLKAQK 1041
 Db 998 dcgncsrifhveklmtnlflimveskgtcpcdt---rlliqaetsdgpdpdcmvqqr 1054

Qy 1042 IRRRPESCHGFHPEENARECGGA---PSLQA---QTVLLLL 1076
 Db 1055 yrkgpdcvcdnnvledytdcggvsglnpslwsiiqgfvlwl 1097

RESULT 1
 US-08-435-675B-5
 ; Sequence 5, Application US/08435675B
 ; Patent No. 5710250
 ; GENERAL INFORMATION:
 ; APPLICANT: Ellis, Steven Bradley
 ; APPLICANT: Williams, Mark E.

Qy 324 REHLDKLFAKGIGMLDIALNEAFNILSDFNHTGQGSICSQAIMLITDGAVDITYDTIFAKY 383
 : : : : ||| : || : : : : : ||| ||| : ||||
 Db 321 KDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRAN--CNKIIMLFTDGGEERAQEIFAKY 378
 Qy 384 NWPDRKVRIFTYLIIGREAAFDNLKWMACANKGFFFTQISTLADVQENVMEYLHLSRPKV 443
 | :|||:|: :|: :||| |||: :| : : : | || | | |
 Db 379 N-KDKKVRVFTFSVGQHNYDRGPIQWMACENKGYEYIIPSIGAIRINTQEYLDVLGRPMV 437
 Qy 444 I--DQEHVWVTEAYIDSTLTDDQGPVLMTTVAMPVFS----KQNETRSKG-ILGTVGT 496
 : | : | || :|: : | :| :||| :|: | :|||:|
 Db 438 LAGDKAKQVQWNTNVDLAL---ELG--LVITGTLVPFNITGQFENKTNLKNQLILGVMGV 492
 Qy 497 DVPVKELLKTIPIKYLGIHGAFYAITNNGYILTHPELRL-----LYEKGKRRKPNYSS 550
 || : : : : :| :| ||| |||:| || : : : :|| :
 Db 493 DVSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKPIGVGPTINLRKRPNVQN 552
 Qy 551 -----VDLSEVEWEDRDDV---LRNAMVNRKTGK--FSMEVK----KTVDKGKRVLMVT 595
 | | : : | :| : || :| : :| : | || : :|| |
 Db 553 PKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVSQDERYIDKGNRT---- 608
 Qy 596 NDYYYTDIKGTFPSLGVLSRGHGKYFFRGNVITIEGLHDLHPDVSLADEW----- 647
 | :| : || :| : : | : : ||| : : : | :
 Db 609 --YTWTVPNGTDYSSALVLPTYSFYIYKAK--IEETITQARYSETLKPDNFEESGYTFL 664
 Qy 648 ---SYCNTDLHPEHRHLSQLEAIKLYLKGKEP-LLQCDKELIQEVLFDA-VVSAPIEAYW 702
 || :|| | : | : : | | | :|| || | : : ||
 Db 665 APRDYC-SDLKPSDNTEFLNLFNEFIDRKTNNPSCNTDLINRVLLDAGFTNELVQNYW 723
 Qy 703 TSLALNKSSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKAGDKENIFNADHFPL 762
 : : : : ||| :| :| :||| :||| : :
 Db 724 S-----KQKNIKGVKARFVVTGGITRVYP-----KEAGENWQENPETYEDS 765
 Qy 763 WYRRAAEQIPGSFVYSIPF--STGPNVKSNNVTASTSIQLLDERKSPVVAAGIQMKLEF 820
 :||: : :||: | :|| : : | : : : | ||| : :
 Db 766 FYKRSLDN--DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNS 823
 Qy 821 FQRKFWTASRQCASLDGKCSISCDDETVCNYLIDNNGFILVS--EDYT-QTGDFGFEIEG 877
 : | | : : : : :| :|| :||| :||| | ||||
 Db 824 WIENFTKTSIRDPCAGPVCDCKRNSDVMDCVILDGGFLLMANHDDYTNQIGRFFGEIDP 883
 Qy 878 AVMNKLLTMGSFKRITLYDYQAMCRANKESSDGAHGLLDPY-----NAFLSAVKW 927
 :| | : : : ||||:| || | | : :| |
 Db 884 SLMRHLVNISVYAFNKSVDYQSVCEPGAAPKQGA-GHRSAYVPSIADILQIGWWATAAAW 942
 Qy 928 IMTELVLFLVEF---NLCSWWHSDMTAKAQKLTLEPCDTEYPAFVSERTIKETTNI 983
 : : | : | : || | : || : | || : : | :| :
 Db 943 SILQQFLLSLTFPRLLEAADMEDDDFTASMSK-----QSCITEQTQYFFDNDKSFSGVL 997
 Qy 984 ACEDCSKSFVIQIPSSNLFMVVDS--SCLCESVAPITMAPIEIRYNESLK CERLKAQK 1041
 | :||: | : : : || :||: | | : : : | : :| :
 Db 998 DCGNCSRIHFHVEKLMNTNLFIMVESKGTCPCDT---RLLIQAEQTS DGPDPDCMVQQR 1054
 Qy 1042 IRRRPESCHGFHPEENARECGGA---PSLQA---QTVLLLL 1076
 | :| : | : | :||| ||| : | ||| |
 Db 1055 YRKGPDVCFDNNVLEDYTDCCGVSGLNPSLWSIIGIQFVLLWL 1097

RESULT 2

US-08-336-257A-8

; Sequence 8, Application US/08336257A

; Patent No. 5726035

; GENERAL INFORMATION:

; APPLICANT: Jay, Scott D

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; APPLICANT: Campbell, Kevin P.

; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

```

; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,257A
; FILING DATE: 07-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 54898
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 238-0999
; TELEFAX: (619) 238-0062
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-336-257A-8

```

```

Query Match          20.3%; Score 1148.5; DB 1; Length 1106;
Best Local Similarity 28.5%; Pred. No. 1.2e-101;
Matches 320; Conservative 235; Mismatches 439; Indels 129; Gaps 39;

```

```

Qy 33 SEQQIPLSV-VKLWASAFGGEIKSIAAKYSGSQLLKQKYKEYEKDVAIEIDGLQLVKKL 91
   || : || : || : : || || | | : || : | : || :
Db 25 SEEPFSAVTIKSWVDKMQEDLVTAKTASGVHQLVDIYEKYQDLYTVEPNARQLVEIA 84

Qy 92 AKNMEEMFHKKSEAVRRLVEAAEEAHLKHEFDADL---QYEFYFNAVLINERDKDGNFLEL 148
   |:::|:: :|::| || ||: ||: | : |::| : : | : |
Db 85 ARDIEKLLSNRSKALVRLALEAEKVQAAHQWREDFASNEVYYNAK--DDLDPKNESEP 142

Qy 149 GKEFI--LAPNDHFNNLPVNIISLSDVQVPTNMYNKDPAIVNGVYWSESLNKVFVDNFDRD 206
   | : | : : | | : : | : ||::| : || : | : : | | | : |
Db 143 GSQRIKPVFIDDANFRQVSQYQAAVHIPTDIYEGSTIVLNLNWTSLALDDVFKKNREED 202

Qy 207 PSLIWQYFGSAKGFFRQYPGIKWEPDE---NGVIAFDCRNKRWYIQAATSPKDVVILVDV 263
   ||::|| |||| | | || | : | : : | | |||| | ||||::|||
Db 203 PSLIWQYFGSATGLARYYPASPWVDNSRTPNKIDLYDVRRPWYIQGAASPKDMLILVDV 262

Qy 264 SGSMKGLRLTIKQTVSSILDTLGDDDDFFNIIAYNEELHYVEPCLNGTLVQADRTNKEHF 323
   |||: || | : : :|| :|| |||| | : :| | | ||||: ||:
Db 263 SGSVSGLTLKLIRTSVSEMLETSLDDDFVNVASFNSNAQDVS-CFQ-HLVQANVRNKKVL 320

Qy 324 REHLDKLFAKGIGMLDIALNEAFNILDNFNHTGQSICSQAIMLITDGAVDTYDTIFAKY 383
   : : : : |||| : || | : | : | : || || || : ||||
Db 321 KDAVNNTAKGITDYKKGFSFAFEQLLNYNVSRAN--CNKIIMLFTDGGEERAQEIFAKY 378

Qy 384 NWPDRKVRIFTYILIGREAAFDNLKWMACANKGFFTQISTLADVQENVMEYLHVLSPKV 443
   | |::|||::|:: :||| ||::: | : : : | || || || |
Db 379 N-KDKKVRVFTFSVGQHNYDRGPIQWMACENKGYEIPSIGAIRINTQEYLDVLGRPMV 437

Qy 444 I--DQEHVVWTEAYIDSTLTDDQGPVLMTTVAMPVFS---KQNETRSKG-ILGTVVGT 496
   | : | || |:: : | : | : | : ||:: :| : | : ||::|
Db 438 LAGDKAKQVQWNTNYLDAL---ELG--LVITGTLPVFNITGQFENKTNLKNQLILGVMGV 492

Qy 497 DVPVKELLKTIPKYKLGIHGAYAFITNNGYILTHPELRL-----LYEEGKRRKPNYSS 550
   || ::: : |:: | :|| ||| ||::| || | : : : :|| :
Db 493 DVSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKPIGVGIPITINLKRKRPVQN 552

```



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/223,305
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,751
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US89/01408
; FILING DATE: 04-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/176,899
; FILING DATE: 04-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-52517
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1086 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-455-543A-54

```

```

Query Match          19.7%; Score 1116; DB 1; Length 1086;
Best Local Similarity 28.3%; Pred. No. 1.6e-98;
Matches 322; Conservative 232; Mismatches 457; Indels 126; Gaps 41;

```

```

Qy  14 ASALLAAAL-LYAALGDVVRSEQQIPLSV-VKLWASAFGGEIKSIAAKYSGSLLQKKYK 71
    | ||| | | : : | | : | : | : | : : | | | | :
Db  3 AGCLLALTLTFLQSLIGPSSEEPFSAVTIKSWVDKMQEDLVTAKTAGSVNQLVVDIYE 62

Qy  72 EYEKDVAAIEEIDGLQLVKKLAKNMEEMFHKKSEAVRRLVEAAEEAHLKHEFDADL---QY 128
    : | : : | | : | : : : : : : : | : | : | :
Db  63 KYQDLTYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASNEV 122

Qy  129 EYFNAVLINERDKDGNFLELGKEFI---LAPNDHFNNLPVNISLSDVQVPTNMYNKDPAI 185
    | : | : : | : | : | : : : : : : | : : : :
Db  123 VYYNAK--DDLDPKNDSEPGSQRIKPVFIEDANFGR-QISYQHAAVHIPTDIYEGSTIV 179

Qy  186 VNGVYWSES LNKFVVDNFD RDPSLIWQYFGSAKGFFRQYPGIKWEPDE---NGVIAFD 242
    : | : | : : : | | : | : | : | : | : | : | :
Db  180 LNELNWTSA LDEVFKKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 239

Qy  243 NRKWIYQAATSPKDVVILVDVSGSMKGLRLTIKQTVSSILDTLGDDDFENIIAYNEELH 302
    | ||| | ||| : : ||| : : ||| : : ||| : : |||
Db  240 RRPWYIQGAASPKDMLLILVDVSGSVGLTLKLIRTSVSEMLETSLDDDFVNVASFNSNAQ 299

Qy  303 YVEPCLNGTLVQADRTNKEHFREHLDKLFAKGIGMLDIALNEAFNILSDFNHTGQGSICS 362
    | | ||| : || : : : : ||| : || | : | : | :
Db  300 DVS-CFQ-HLVQANVRNKKVLKDAVNINITAKGITDYKKGFSAFEQLLNYNVSRAN---CN 355

Qy  363 QAIMLITDGAVDTYDTIFAKYNWPD RKVRIFTYLGREAAFDNLKWMACANKGFFTQIS 422

```

```

      : ||| ||| : || ||| |:||:| : :| :||| |||: :|
Db 356 KIIMLFTDGGEEAQQEIFNKYN-KDKKVRVFRFSVGQHNRYERGPIQWMACENKGYEIP 414
Qy 423 TLADVQENVMEYLHVLSPKVI--DQEHVWVTEAYIDSTLTDDQGPVLMTTVAMPVFS- 479
      : : : | ||| || || : : | : | :| : : | :| :|||
Db 415 SIGAIRINTQEYLDVLRPMVLAGDKAKQVQWTVNYLDAL---ELG--LVITGTLPVFNI 469
Qy 480 ---KQNETRSKG-ILLGVVGTDPVKELLKTIPKYKLGIGHYAFAITNNGYILTHPELRL 535
      :|:| | :|||:| || : : : :| :| :|| ||| |||:| |||
Db 470 TGQFENKTNLKNQLILGVMGVDVSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPNL-- 527
Qy 536 LYEEGKKRRKPNYSSVDLSEVEWEDRDDV-LRNAMVNRKTGK--FSMEVK---KTVDKG 588
      : :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 528 -----QPKPE--VTLDFLDAELENDIKVEIRNKMIDGESGEKTFRTLVSQDERYIDKG 579
Qy 589 KRVLVMTNDYYTDIKGTPFSLGVALSRGHGKYFF-----RGNVTIEEGL- 633
      | :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 580 NRT-----YTWTPVNGTDYSLALVLPY-YSFYIKAKLEETITQARSKGKMKDSETLK 632
Qy 634 -HDLEHPDVSLADEWSYCNLDLHPEHRHLSQLEAIKLYLKGEKPE-LLQCDKELIQEVLPD 691
      : | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 633 PDNFEEGSGYTFIAPRDYCN-DLKISDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLD 691
Qy 692 A-VVSAPIEAYWTSALNKSSENSDKGVEVAFLGTRTGLSRINLFVGAEQLTNQDFLKGAD 750
      | : : ||| : : ||| :| :| :| :| :| :| :| :|
Db 692 AGFTNELVQNYWS-----KQKNIKGVKARFVTDGGITRVYP-----KEAGE 733
Qy 751 KENIFNADHFLWYRRAAEQIPGSFVYSIPF--STGPNKSNVVTASTSIQLLDERKSPV 808
      : :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 734 NWQENPETYEDSFYKRSLDN--DNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLK 791
Qy 809 VAAVGIQMKLEFFQRKFWTASRQCASLDGKCSISCDDETVCYLIDNNGFILVS--EDYT 866
      | ||| : : : | :| :| :| :| :| :| :| :| :| :|
Db 792 PAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVILDDGGFLLMANHDDYT 851
Qy 867 -QTGDFGEIEGAVMNKLLTMGSFKRITLYDQAMCRANKESSDGAHGLLDPY----- 918
      | | |||| :| :| :| :| :| :| :| :| :| :| :|
Db 852 NQIGRFFGEIDPSLMRHLVNI SVYAFNKSYDYQSVCEPGAAPKQGA-GHRSAYVPSVADI 910
Qy 919 ---NAFLSAVKWIMTELVLFLVEF---NLCSWWHSDMTAKAQLKQLEPCDTEYPAFV 971
      : :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 911 LQIGWATAAAWSILQQFLSLTFPRLLEAVEMEDDDFTASLSK----QSCITEQTQYF 965
Qy 972 SERTIKETGNIACDCSKSFVIQQIPSSNLFMVVVD--SCLCESVAPITMAPIEIRYN 1029
      : | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 966 FDNDSKSFSGVLDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPCDTRLLIQAEQTSQDGN 1025
Qy 1030 ESLKCEKRLKAQKIRRRPESCHGFHPEENARECGGAPSLQAQT--VLLLLPLLLMLFS 1084
      : :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 1026 ---PCDMVKQPRYRKGPDVCFDNNVLEDYDCGGVSGLNPSLWYIIGIQFLLWLVS 1079

```

GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2001, 13:33:21 ; Search time 392.32 Seconds
(without alignments)
404.352 Million cell updates/sec

Title: US-09-397-550-22
Perfect score: 5667
Sequence: 1 MAGPGSPRRASRGASALLAA.....SLQAQTVLLLLPLLLMLFSR 1085

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 901707 seqs, 146207799 residues